

APPENDIX

BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 7071378_SEQ_1 check: 9103 from: 1 to: 531

WPDEF ESR1 PRO - disclosed, not patented; ESR 1 of Figure 4

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	162	Length:	39
Ratio:	4.154	Gaps:	0
Percent Similarity:	69.231	Percent Identity:	69.231

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 5
. = 1
```

1587_SEQ_1 x 7071378_SEQ_1 December 15, 2006 16:23 ..

```
199 tttactaaaattttctctgtatagtaacatgtcataact 237
    |||| |||| | ||| |||| || |||||
355 tttattaaaactgtcttaaaataggccaagtcataaat 393
```

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0

1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1 gaattcgccc ttggtagatg tctagatgac ctattctact ttctctaaga
51 ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta atagggtcca
151 agaaccagcc acaatccatt tattagtctc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa ctgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttgg
```

351 tgtcttcggtt tttaaactta gttgtatttt tttcttagt tctgtccttc
401 tagtggtata gagcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaaag gccagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagctca ggggaccatg

Input Sequence: 7071378_SEQ_1

!!NA_SEQUENCE 1.0
WPDEF ESR1 PRO - disclosed, not patented; ESR 1 of Figure 4
7071378_SEQ_1 Length: 531 December 15, 2006 16:20 Type: N Check: 9103
..

1 gatcattaag gactaagcag tctttttccc tttcggttg catcatcttt
51 agtcttcacg actattataa gccgaagcta ttaccacctg gctatagctt
101 cgggtgttcac ctttattatc ttccgactat gtcttcacct tgtataacct
151 tgtcttgggg gaaaaccttc atcctgaagc cgaagctccc tgtaataatt
201 catatcatgc taaaaataaa tggtcagtcc tgttttttag gaccttcgga
251 agaggaaggc cccccaacaa gacgattaac tagtattgtc tactgcatt
301 gtttttttgg cacttcatca ataatgcctc aatagcatac ttcattttag
351 gaactttatt aaaactgtct taaaataggg ccaagtcata aattcattca
401 aagtgactct tcattttctta ctctctatct ttggtggttt tgtatatata
451 tatgttcacg gttgagtgat gttcctacac cactacacca cacgttagat
501 atatatacag aaaatagctt cactatctag a

BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 7071378_SEQ_2 check: 806 from: 1 to: 2493

WPDEF Bonello patented promoter; ESR 2 of Fig. 4 begins at position 1986

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	139	Length:	31
Ratio:	4.484	Gaps:	0
Percent Similarity:	70.968	Percent Identity:	70.968

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 5
. = 1

```

1587_SEQ_1 x 7071378_SEQ_2 December 15, 2006 15:59 ..

```

      .      .      .
526 agtatactccaagcacatttgaatttgatt 556
    | | | | | | | | | | | | | | | |
525 attttagaccaaaccattttaatttggttt 555

```

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0

1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```

1  gaattcgccc ttgtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatctgccc
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtctc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggg acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttgg
351 tgtcttcggt tttaaactta gttgtatttt ttttcttagt tctgtccttc

```

401 tagtggtata gagcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcga ggggacccatg

Input Sequence: 7071378_SEQ_2

!!NA_SEQUENCE 1.0
WPDEF Bonello patented promoter; ESR 2 of Fig. 4 begins at position 1986
7071378_SEQ_2 Length: 2493 December 15, 2006 15:57 Type: N Check: 806
..

1 aagcttttcc ggtgatgaag cacctgtaat acttaacagc atgctgaaaa
51 caaatagtta gctgtgtttt tgaggacctt cggaagatga agggccccc
101 cacatcccat gcatcaagtc cccatgactt gcaaaaaagc aaattttatc
151 aaaatttttc ataaaacact tgaacacatt tctctttttg aaaagtgtag
201 agcactagca actgtctact aaaaagggtc ccaaatctct gggtataaca
251 atcgcatggg aaataacaca aagggaatcc tactaagagc agtaatttgg
301 ctaaaacaat agtgagcatt ttaatgtaat agggaatagg agcatgcaat
351 acttgtgttc ttccagggtt ttgatgtcct caaaagtgtg ccccccctggg
401 gcagttgcaa cactcaaaat ctactcgtat acataaagaa acatgggcac
451 aaaaataagaa acaatactca aattatgaaa aaggttcaaa tggctctata
501 attattgtag acattttaga atttatttta gacccaaaacc atttaaat
551 ggttttaaat gagtttagata ttaatattta ttcagtttat agttatttgg
601 gacatttatt tacttaacta taacttctag ggttttataa gtaaatattg
651 ggtccctagt tggaactagc tcagattgct ggttgatttc cataaaagtc
701 gaggttcctt tagcaaaaaa ccacggtgaa caagggggag atagggtgtg
751 accgatattc ctaaatattg atcgttggac ggcacatgga tgtctcagat

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801 taaatggtgg atgtgcaagc gacgcgcaca cgatggagga atggcttcac
851 gacgggtggc tactagagct ggctacgtca accaatggag ggctcgggtca
901 aggtcaaaat ttgttgccaa gccactgtgg ctcacgatga gtcgattgag
951 cacatatcaa ggtcgagggt caaccagagg ggcaagatcg atggtgcagt
1001 ggtgttctcg atggaagggg aaacttcggt gagcaattca agatttccta
1051 tcatgtgacc gggtcaggga atgggcgcat ggggtttggt accttctggt
1101 gcacatcatg ttgctgtatc gatgtcaagg gagcattagg gttcacgagt
1151 cagcgatgac gggcatgggt ggacttgtgt caccatgggt cgatcaacta
1201 gggacgatag agctctatga agtttcacaa ctctctcaca ctctagggat
1251 catggtgaca aaggtgggga ggacggggcg tctctagtga gggtggaatg
1301 cagttctgtc acgtgggaat agtggcggca tcgcttgtaa tgaataaaag
1351 gtgcttgggt ggctgggaag tgcaatatga gggaaagtag tggtcggggg
1401 atgttccttt tataagggag caccattgat taatggaaga caatgacaca
1451 aagggtggtg cgacagttta aagctcgaat gctgctaggg gtgctcaagg
1501 ttaaaagatc aggcacaggg gaggaaggcg agggataaaa tttctttact
1551 ccagttgtgg ggtgatgggg acaagggtag tgctcaagca agggagggcg
1601 agttcagcgc agagatgcct gttgtgacac atgggggggg gggaattgga
1651 ggttgggggt gaccagggtga cgttatggcg tgaccacagag aagagaccca
1701 ctgatgggga aaaaagggtc caacagggtg ggaccaaggt gtcagtgact
1751 caccgtgaca tgttattgga aagttacgtc cggaatggtt tgggcctgag
1801 tgatctaggc tggctcgggc actgtgctga tcctttaatt tctccattcc
1851 caatttaagt tgaattttta attcaaatca aatgactcca aatctctcca
1901 aaattaccaa aatatagaat atttagatga atatgttggt ggagtttggg
1951 ctccgctttt ggtagtatg tttgtataaa aataatttct ctccctttgt
2001 cacttccaat attgacttaa atttttatgt agcaatgcca acttttttta
2051 gtagtgtgcc acttatagca caaaaactat atccatttct taatagtccct
2101 tgaaatccac attctatttt tagccattct tcaaaattgg cacaaaacta

2151 ggaaaaattta atacattctt gccataacat attctagtgc aaatgttaac
2201 tagattgctc aatattagca aacttctttt gtaagattca ttaatatgtc
2251 tacattgcat acttttttag aagttcatca ataatgcctc attagcatac
2301 ttcatatttag gaacttgatt aaaaccgcct taaaatagag ccaagtgacg
2351 gatccattta aagggtgattc ttaatttctt acttcctatc ttggtggct
2401 tatgtttata tatgtgtggg tggttgaatg atgttcctac accactacac
2451 cacacgttgg acatatatat ggaaaaatagc ttcacagtct aga

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 7071378_SEQ_3 check: 9984 from: 1 to: 1708

WPDEF ESR 3 PRO - disclosed, not patented; ESR3 of Fig. 4 begins at position 1193

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	165	Length:	45
Ratio:	3.667	Gaps:	0
Percent Similarity:	66.667	Percent Identity:	66.667

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 7071378_SEQ_3 December 15, 2006 16:24 ..

```
      .      .      .      .
199 tttactaaaattttctctgtatagtaacatgtcataactgaact 243
    |||  ||||| |||  |||  || |||| || | |||
1529 tttatgaaaattgtcttaaaatagggccaagtcacaaatccactt 1573
```

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0

1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt
201 tactaaaatt tttctctgtat agtaacatgt cataactgaa ctgtgtgagaa
251 aaacgccagt tatttatggg acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttgg
351 tgtcttcggt tttaaactta gttgtatttt ttttcttagt tctgtccttc
```

401 tagtgttata gaggcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaaag ggcagcagct taataaacct tttatattag
501 ttcaaaaagga caccagtcta taaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcga ggggaccatg

Input Sequence: 7071378_SEQ_3

!!NA_SEQUENCE 1.0
WPDEF ESR 3 PRO - disclosed, not patented; ESR3 of Fig. 4 begins at
position 1193
7071378_SEQ_3 Length: 1708 December 15, 2006 16:22 Type: N Check: 9984
..

1 aagcttagaa attttaaaaa aagccaggca agcgttggtg tgcaaaagagc
51 taaaaattag gaagacaaga gaacacggca agaaagcatg ctaaaatgtgc
101 tcgcggtgcg ttcttattta tacgtcgaat acgttgcaag tggtagggcc
151 ccacttgta ttgactattg ctattctagc aaagggaagg tgtttttcgg
201 accttcggct taaggccttc gtccatctcg caatctgaat ttatcattct
251 acaaaattaa tattgtgagg ggctactgtt gggggccttc gacttcggaa
301 ggtcctcaaa aactgggtta acagtgttct tggagtataa tgcataaaca
351 ggtatcttcg ggtttggatc agaactacaa catgaagagg cacaagaac
401 acgaagggtg gcgcagagcc gaagctcacg tgtaggagag ctcgggcacg
451 acagcagaaa aagggaaccg acttaaaagg aaaggctatt cagacctoga
501 tggatttcta taggtcatta gcaaatgtaa agggcatgaa tgtaatttta
551 catgggctgt gtccttgctc ataaatagat gaacagtact ctgcgtactgt
601 tcacgtgac ttggcattcg ctttttgcac cagcgttgta cccttgcttt
651 ccttcaaacg gaaggatcat ctataatttg ttattgtgtt attgtggata
701 tggtaatgca aataaaaaa agttgatgat aatgtttata ttatttttcg

751 tatttcatat atgaattctt cctcatcatt tattgtgctt acgaaggttt
801 ttccttcaaa atctttgtcc ggaattcatt atatccgaag ggaaataaatg
851 tctcgaagga cgaaggactt tgatatTTaa cacttttcat gttgccttgt
901 tcttgactct tagcatttga gaacaagtcc ccaacagctc ctaagctctt
951 ctttgaagaa acaactacta gatgaagttt ctccaaaagt acgtccattg
1001 aatggagtaa agagtcattt gacctctcg gataaaaatta aaatgagaat
1051 aagtaagaat aaaacacctc tattatcaaa tctaggccat acaaacattg
1101 ggtattacta aaaaatagct aatgccatct ttcaacattt ggaagttaaa
1151 accaaccaat cctcactcat tcccaagaaa tattggatca tatttaacat
1201 tttgtgtcac ttacaaaaat ggcttaatct tttatgcggc aatgccaaac
1251 ttttttagca gggtgccact tgtaacatga aaactataac tttttcaaa
1301 tagtaccttg aaattcgcat tctattttta tgcattcttc aaaattgaca
1351 caaattaaac taggagaatt caatacatc ttgccataac atattctaatt
1401 gcaaatatta agtagattgc tcaacatcg tacacatctt ttggacgatt
1451 aattagtatt gtctcactac attctttggt ttagcagttc atcaataatg
1501 cctcaatagc atacttcatt ttaggaactt tatgaaaatt gtcttaaaat
1551 agggccaagt cacaaatcca ctccaagggt gactcttcat ttcttacttc
1601 ctatctttgc ttgtttttgt atatatatgt gtggatggtt gagtgatgtt
1651 cctacaccac tacaccacac cttagacaca tatatggaaa atagcttcac
1701 tgtctaga

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BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_1 check: 2029 from: 1 to: 4305

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	169	Length:	67
Ratio:	2.770	Gaps:	2
Percent Similarity:	72.131	Percent Identity:	72.131

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

1587_SEQ_1 x 6777591_SEQ_1 December 15, 2006 17:07 ..

```

      .
161 acaatccatttattagtttcataataatgcata...aattttta...ct 204
   ||||| || | || | ||| ||| ||| |||
956 acaatcaatatgataataataataataataataatcaattattaatct 1005
      .
205 aaaatttttctctgtata 221
   | ||||| | ||||
1006 acaattttttaattata 1022
```

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0

1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```

1  gaattcgccc ttggtagatg tctagatgac ctattctact ttctctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta atagggtcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggg actttaagct ggtgccctca gttttgttgg
```

351 tgtcttcggtt tttaaactta gttgtatattt tttcttagt tctgtccttc
401 tagtggtata gagcataagg acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcaa ggggaccatg

Input Sequence: 6777591_SEQ_1

!!NA_SEQUENCE 1.0
6777591_SEQ_1 Length: 4305 December 15, 2006 17:05 Type: N Check: 2029
..

1 ttcaaaaccc gattcccgag gcggccctat tgaagatat ggggaagttc
51 gacgagatcg atgtcgggtc gagtgcctat gtgatggtgc cgtttggggg
101 gaggatgagc gagatagcca agactagcat tccgttccca cacagagtgc
151 ggaatttgta ccaaatccaa cacttgctgt attggagcga cgataggagc
201 gcggaaaaac acatccgttg gatcaggagg ttgtacgatg atctcgagcc
251 ttatgtgtcg aagaatccga ggtatgctta cgtgaactac agggatctcg
301 acatcgggat gaatggagga ggtgaagggg atgagaaggg tacttatggt
351 gaggctaagg tgtgggggga gaagtacttt ggggtcaact ttgatcggtt
401 ggttcgggtg aagacgattg ttgatcccaa taatgtgttt cgaaacgagc
451 agagcattcc ctcaattcca actcggttat aaggatcaat gatcaatgag
501 aattttcctt tccaatgtga ttacaagttc tattgggtca gctttctcaa
551 ctgctcctat tcatttagat taattcataa caactattaa ttaccagcc
601 ttttatccgg cccgttgccc gatttatatt cttaagtatt agatgaaatg
651 aaaccgattt agtttttatt gagatgagat taatcttaat ttgcttgaaa
701 tttaactcacg gttgatgtga tatttggaat taactaaaaa gataaatatc

751 ggataaaaaat aaaaatattt aaaataaata acataaacat aagaacaata
801 aaataaataa atttaatttt aattttatttc ctgtttttct ttctgtatca
851 tacatctctt ctcttacttc ttaaaggctt ttcaattatc acttaattaa
901 atacaataga taaatcggtt attctataac attaacctat acacttgac
951 ggtgaacaat caatatgata atataataat aatataataa ttcaattatt
1001 aatctacaat tttttaatta taaagtttat gcggtcagtt tctgcaagct
1051 ccgagctcct tgtcatcggt agtttctgcg gtctcaaggt ataacgactc
1101 ggagcgacga gccctttgct tccaatggac ggggtgcatt tctgccgtcg
1151 ttgagctcga ttggcgtgtc atgctggagt cagagttcct aaaaaaaaaac
1201 cctaaactag aggggtgatta gggtgaaatt aggggtgttg cctgggttcc
1251 attgtccaaa gtttttagtca acttaaaaac agacttaaat tttatgcttc
1301 aaaaatagttt atctgttatt atattagcgt gtaattagtc ttgacaatgg
1351 ggccgggacgg gtacggattc ggggacccga tccccgccca tagtgtaatg
1401 gctcaactgc caagtcagca ttggaccgaa attattggac acgaagtact
1451 aatgtgaaaa actttacatt tgttattttc tactttaata ctatgctatt
1501 ttcaaaattt gaactttaat actatgtttt tatatagttt agtatatctt
1551 aattttttatg caaattcatc taattgtatt aaactatttt cgatccgtag
1601 ctaattattt cgaaggcaag tcaaagtgtt attgtggact atgtgagcta
1651 atattgaacc tttatctctc ccaaccactc aagttaattg aaaccaactc
1701 gatcggttgg gtttcgagct atttcgagcc attgttgta tatgcacgtg
1751 agatatcaag attgaccga acactttatt atgataatgt agaaaaagaa
1801 aacatattct aagactacat gcatgcaaag tgcaacccct gcatggaaag
1851 ctgctcaaca cgtggcatag actcccgcca cgtgtccatt ccacctcatc
1901 acctcacccc caccgttcac ctcttattat atcacacaaa tcaatcaatc
1951 ctactctctc atactcgaac aaatccgacc aacttatacc aatattccca
2001 aacttgatta atttctcagc aatatggatc agacgcacca gacatacgcc
2051 ggaaccacgc agaaccgag ctatggcggc gggggcacia tgtaccagca

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2101 gcagcagccg aggtcttacc aggcggtgaa ggcggccact gcagccaccg
2151 cgggtggatc cctcatcggt ctgtccggtc tcatccttac ggccaccgtc
2201 atttactca tcatagccac cctctcctt gtcattctca gccctgttct
2251 tgtcccggtc ctcatcacgg tcgggtcctt gatcacccgg tttcttgctt
2301 ccggtgggtt cggagtcgcc gccgtcacgg tcttgtctg gatctatagg
2351 tatgtataag ctttggactt tagtattggt ataaaaatac taagctgatt
2401 tatgaacatg gatctcccaa caagagttat ttaaatgcat tctcggctcg
2451 actcgatcgg ttgggttttg agctactcgg tcacaatggc cgggtcggct
2501 ctggatctgt tatactaata tttggaagcc tgaagttca tttgtctgcc
2551 ccaacttccc actacctttt gaggggtgta agaagccata caaactaatt
2601 atgaatccct cccaacaact cagaactcga gtcagtggtt tgtgacggtt
2651 ctctataaac atttcgaaaa tctttgttca atgaacgtag aaatgacct
2701 gcttgatgat tgtgggtctt ataaggtacg tgaccggcgg gcaccggcgg
2751 ggaggggatt cgctggacca ggctaggctg aagctggcgg gaaaggccag
2801 ggaggtgaag gacagggcgt cgaggttcgc acagcagcat gtcacagggt
2851 gtcaacagac ctcttaaaga gagtccctca gttaaattgg tcttcgtttc
2901 tgtttcgtgg cggcttgtaa actctctttt aagtgtgctg tttctctttt
2951 gtctcgtgtg ttgtaagtga aagtgtaatc gaagttccaa gttggagatg
3001 tttgtaacga tgatgttttc taataatcag agatattaaa aggggtgcta
3051 atttagtatt gcgtctgata tcggacccaa ctcgcaagta aaattgcaga
3101 ggatgagttg tacagaacaa gcgtgcattg ttctggaagt tcatctcctt
3151 ggagccgacc ttgttgcttg cagtttcgcc aagtccacta gacaatgtta
3201 cgagttaagc ctctgtcaaa cagatcgctc tagcgtccca gaaaacacca
3251 gatttttcca aaaccatcgg ggatcaattt tcgattcaat tccgatcttg
3301 gaagtacttg aacagaagca tgatgctaaa agataataga aaatcgaagc
3351 ctagaaaagt tgtacagaaa gcaacaagtc aaaaatatag atcaacttca
3401 aaggttcaaa ttacatctta cagaccccaa aaaatgacag ttaacagaag

3451 tcgactaaac agaaccagc cagcttcacc tggaatgaag gagctttgat
3501 caatccatcc tagcttcatt cccctttgaa attgcagaca gagctctcat
3551 cctgctaaag ctggtggctt attcttaacc ctgcaatcaa taagcatgaa
3601 ctaacattgg acaccttcac cggcggattg ctcgaaaatc agtgagcgag
3651 ggattttacct gtgtgtgtag taacctctct ccttgtagat aaaatctgga
3701 aattccggca tcaactactg ccacctttct gcttaagggtg attttatcac
3751 caaggctgag cgtgattcct tgcgtcttgc tccgaatcct gatgtatcca
3801 ctgagctttc catctccttc cttctccagg cttatgttca ccaatgcgtc
3851 ctgcccgaac acactcttgg cgtacaagtt cgcagccagg aatccacact
3901 ctccatcaag tgcagacctg caaaccccaa ataagaacac aaactccaaa
3951 gtcaacgata aattctccgc cttttatgaa gaaaaggaaa cttctgggta
4001 cttacgggtgc cgtcagacac ttcataattg tagacttgat gatatggtcc
4051 aggaattcct tctcgttctg aattgttgtg ttaacagcaa cctgacagac
4101 agaaagatat cgcaaattta agatactggg atgactaggc acagagaaat
4151 gaaatctaata tctagaagta aaaccttatt ttccattca aattctgccc
4201 acatagtccg gaacgcagca tccgagcaag aagcaggaga gatgtaatcc
4251 atgatatcga tgtggatata gttgaggacg acaactgaac gttccatcac
4301 attgg

BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_4 check: 8952 from: 1 to: 3501

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	134	Length:	21
Ratio:	6.381	Gaps:	0
Percent Similarity:	80.952	Percent Identity:	80.952

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 5
. = 1

```

1587_SEQ_1 x 6777591_SEQ_4 December 15, 2006 17:08 ..

```

      187 atgtcataaatttttactaaa 207
      ||||| |||| |||| |||
     2977 atgtcagaaatccttacgaaa 2997

```

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0

1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```

1  gaattcgccc ttggtagatg tctagatgac ctattctact ttctctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgta gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtttc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa ctgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttg
351 tgtcttcgtt tttaaactta gttgtatttt ttttcttagt tctgtccttc
401 tagtgttata gagcataagg acaaaattga gcaaaaaatg actaaggata

```

451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcac ggggaccatg

Input Sequence: 6777591_SEQ_4

!!NA_SEQUENCE 1.0
6777591_SEQ_4 Length: 3501 December 15, 2006 17:05 Type: N Check: 8952
..

1 tctagacatt tgacataaac cgaattcaaa gaacacaaca ttgactaaca
51 ccaaaaagaa atagagtagt gaaatttggg agattaaaaa atagaacaaa
101 actgattctt agaagaaga gatgattagg tgctttcagt tcggtctgtc
151 aggaaatcga gatgttcaat tatttacatt gtcgattcat ctcccaattg
201 tcctggttcc tttactgtcc gacgcttttt tgaatcccag ttaattccca
251 tcaagtcttc cttcagctgc gtagcactgc tagctccaac atggagcgtg
301 gagtctactc gttcattggg catcgcaaa ggttgccctc atgttctgct
351 accagccagc gccaccgcc tcttggttgt gtggacaatt gcggtgaagc
401 gcgcaagttg acatcccata gtctcgacac ttcaccatat ggatgtttaa
451 aacgtatata acgagtgcga tctacatgct ccatcacacc acataataag
501 caatagtttg ggagcttttc atatttgaaa cgggcattga cgacttgccc
551 tctcgataat ttaatctttt tttctcttca gctgattgtg tgcattccatt
601 cgggctcaga agcacatcaa agggatctct ccatcgtagt attgggtcgt
651 gtcgtatgat acgaagcagt cgatgaagtt tcctaattgtg cgagctacag
701 gctccgcaaa gaaccgcga ggtagatcgt atgctagtac ccaaaaatca
751 gtttgtcgta gcggaatcaa cactagagac tcaccctaata gcatctcatg
801 tgtgatgaac agtttatcat ttgtgagtct aggggtcatt gtcgatgacc

851 caatgcacat tgagcttatg atagaatttg aataggaagc gttttccacc
901 cagatcacga atagctaccc ctttttcggg cgccaaattt ccggcatcct
951 atcttccacc acaactaaa gatgcatcg gtaaggaact caccgaccac
1001 acacatcgaa taatcttcgg tgaccggttc ctgttgatca agtcctca
1051 tttcctcaac ctagtcttca atcgccgcta gcgttatccc ccgcatatgg
1101 actttcatag cgcgaggcgt agccggagac gacgagcaag aaggatgagc
1151 ggcggcagat tgcggctaaa gaaacgagct tcctgccttg ctctatggag
1201 gcagatttct gagttgatgg tgatggattt gtgatgtgga cacttttaat
1251 ttaagttgat tttttagcac ttcatcagc taattaaata aataatttcc
1301 agtattttat atttatttcc ttacgttato taattttttg aaagattaaa
1351 actttgatat agccaagatc atgacacgtc gaagttaagt gaatgagact
1401 cctaacaagg taataacaaa gcagttcata aaccgaatga ccttgatctt
1451 tactaagctt gagatcattg aacatataat taaatacgtt aatgaaagat
1501 aagaacttta atataaaaat cattcaaaac gagaaactga taacaaaaac
1551 aaagcaaacg gccacaaaaa taatagacgg tggaaggatg atgcagagcc
1601 atccaccctt ttttccagt ttcttactg ctactttctc tatgcatac
1651 acaagacgcc cttgaaactt gttagtcatg cagagccctt actcgccagg
1701 tcaccgcacc acgtgttact ctatcacttc tctcccttt cttttaaaga
1751 accaccagc cactccctc tcacaaacac tcataaaaaa accacctctt
1801 gcattttctc caagttcaaa ttagttcaca gctaagcaag aactcaacaa
1851 caatggcgga tcgtacaaca cagccacacc aagtccaggt ccacaccag
1901 caccactatc ccaccggcgg ggctttcggc cgttatgaag gtggactcaa
1951 aggcgttcca catcaccagc aaggatcagg cagcggccca tcagcttcca
2001 aggtgttagc agtcatgacc gcgctcccca tcggcgggac cctccttgcc
2051 ttggccggga taaccttggc tgggacgatg atcgggctgg cgatcaccac
2101 cccgattttt gtcacttgca gccctgttct agtcccgccc gctctgtcga
2151 tcgggtttgc cgtgagcgcg tttctggcct cggggatggc cgggctgaca

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2201 gggctgacct cgctgtcgtg gtttgcgagg tatctgcagc aggctgggca
2251 gggagttgga gtgggggtgc cggatagttt cgagcaggcg aagaggcgca
2301 tgcaggatgc tgcgtgggtat atggggcaga agaccaagga agttgggcag
2351 gagatccaga ggaagtctca ggatgtgaaa gcatcagaca aataaggtga
2401 taataagggg ttttgggttc gtgtgtaaac tggtaaaatg gaaattctgg
2451 gttttactgt acttttgcac gtagtggaat gaatgagttc ttgttctctt
2501 ttgtctttta atcataaagt aagaagcagc atttcatgtt ctggttgaat
2551 attgtcaaga attcgcaaca aatttagcta aaccagtcca atcttaccgg
2601 ttagacgact tcccagtaag aaacattcca ggtccatccc ggtataagag
2651 tctggacttc tgaaaccttt agaccttga tttgaaaaa agatgaaacc
2701 tttagaataa attacaacga tggcagattg taaaaaactg gtagtcgagat
2751 catgtaaatt agcccataac taagaaccgg cgatgacaac aattactagg
2801 aatatggttg ttgggctggt cggcggctag cggtgatgat ttggaagaat
2851 cgggcatcca gaatgtgaga accgaatcat cgacgaacat taccggcgga
2901 ggagccatt tcaagcaact ttggaactcc tatatggctg ttccagcagg
2951 ccacctgctc aagaaagaaa gaagccatgt cagaaatcct tacgaaatct
3001 aactggatgc tgatatgaat ccgccagggtg tgcggagttc ttacaggca
3051 ggatctataa agaagaaaca tgttttgat tggcattgtt gatgttccaa
3101 gcacgcagcg atctatctcc ggatcctaac aaaaaaata cggattctgt
3151 aagaacaag cgcagaaaac ttctgcaacg aaaccactcg tatatttggt
3201 tctgagttgg agaagatga ccatactact gtatttggtt gaacttggat
3251 tggaaaccgaa attttgagtt gaaaacgag tgatcgata taaatttcag
3301 attcagatta ggatataccta tgagagaagg tagagttacc tgatactaca
3351 tactgcccac caggggtaaa agttgcctcg atggtttgtt ttggagatgg
3401 ttccaggcta aatccacaac gctgaacaaa ttaaaagatg aatggatcaa
3451 tcttcaaccc ttacttctgc atttatgagg attggctcaa ggctctctag
3501 a

BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_6 check: 6664 from: 1 to: 1676

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	169	Length:	34
Ratio:	4.971	Gaps:	0
Percent Similarity:	73.529	Percent Identity:	73.529

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 5
. = 1
```

1587_SEQ_1 x 6777591_SEQ_6 December 15, 2006 17:08 ..

```

      343  ttgttggtgtcttcggttttaaaacttagttgta 376
            | ||| || |||| ||||| ||| |||
1617  tatgtatgtttcttggttttaaaattaaatgga 1650
```

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0

1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```

1  gaattcgccc ttggtagatg tctagatgac ctattctact ttctctaaga
51  ttttctctgt atgagtaacc tgcataatt taacttgta gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtctt atataaatgt cataaathtt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa ctgtgagaa
251 aaacgccagt tatttatggt acgggattaa taggttccaa aaaccagccg
301 taacctattt atattagggt actttaagct ggtgccctca gttttgttg
351 tgtcttcggt tttaaactta gttgtatttt tttcttagt tctgtccttc
401 tagtgttata gagcataagg acaaaattga gcaaaaaatg actaaggata
```

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451 aaaatgagga tatcagaaag ggcagcagct taaaaaacct tttatattag
501 ttcaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcac ggggaccatg

Input Sequence: 6777591_SEQ_6

!!NA_SEQUENCE 1.0
6777591_SEQ_6 Length: 1676 December 15, 2006 17:06 Type: N Check: 6664
..

1 tccactatgt aggtcatatc catcatTTTA atttttgggc accattcaat
51 tccatcttgc ctttagggat gtgaatatga acggccaagg taagagaata
101 aaaataatcc aaattaaagc aagagaggcc aagtaagata atccaaatgt
151 acacttgTca tcgccgaaat tagtaaaata cgcggcataT tgtattccca
201 cacattatta aaataaccgt tatgtattgg ctgcatttgc atgaataata
251 ctacgtgtaa gcccaaaaga acccacgtgt agcccatgca aagttaacac
301 tcacgacccc attcctcagt ctccactata taaaccaccc atccccaatc
351 ttaccaaacc caccacacga ctcacaactc gactctcaca ccttaagaa
401 ccaatcacca ccaaaaaatg gcaaagctga tgagcctagc agccgtagca
451 acgcagttcc tcttctgat cgtggtggac gcatccgtcc gaaccacagt
501 gattatcgac gaggagacca accaaggccg cggTggaggc aaggtggcag
551 ggacagcagc agtctcgag cagcagatcc agcagcgaga cttctgagg
601 agctgccagc agttcatgtg ggagaaagtc cagaggggag gccacagcca
651 ctattacaac cagggccgtg gaggaggcga acagagccag tacttcgaac
701 agctgtttgt gacgacctta agcaattgcg caccgcggtg caccatgccca
751 ggggacttga agcgtgccat cgGCCaaatg aggcaggaaa tcacagcagca
801 gggacagcag cagggacagc agcagggaag tcagaggtgg atccagcaag

851 ctaaacaat cgctaaggac ctccccggac agtgccgcac ccagcctagc
901 caatgccagt tccagggccca gcagcaatct gcattggttt gaagggtga
951 tcgattatga gatcgtacaa agacactgct aggtgttaag gatggataat
1001 aataataata atgagatgaa tgtgttttaa gttagttaa cagctgtaat
1051 aaagagagag agagagagag agagagagag agagagagag agagagagag
1101 agaggctgat gaaatgttat gtatgtttct tggtttttaa aataaatgaa
1151 agcacatgct cgtgtggttc tatcgaatta ttcggcggtt cctgtgggaa
1201 aaagtccaga agggcgggccg cagctactac tacaaccaag gccgtggagg
1251 agggcaacag agccagcact tcgatagctg ctgcgatgat cttaagcaat
1301 tgaggagcga gtgcacatgc aggggactgg agcgtgcaat cggccagatg
1351 aggcaggaca tccagcagca gggacagcag cagggaagtg agaggtggtc
1401 ccatcaatct aaacaagtcg ctagggaact tccgggacag tgcggcacc
1451 agcctagccg atgccagctc caggggcagc agcagtgctg atggttttga
1501 agtgggtatc gatgagatcg tataaagaca ctgctaggtg ttaaggatgg
1551 gataataaga tgtgttttaa gtcatgaacc gtaataaaaa gagagagagg
1601 ctgatggaat gttatgtatg tatgtttctt ggttttttaa attaaatgga
1651 aagcacatgc tcgtgtgggt tctatc

BestFit Results

BESTFIT of: 1587_SEQ_1 check: 9861 from: 1 to: 590

to: 6777591_SEQ_8 check: 1234 from: 1 to: 4999

Symbol comparison table: swgapdna.cmp CompCheck: 2335

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	445	Length:	379
Ratio:	1.233	Gaps:	7
Percent Similarity:	61.224	Percent Identity:	39.650

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 5
. = 1

```

1587_SEQ_1 x 6777591_SEQ_8 December 15, 2006 17:09 ..

```

      .      .      .      .      .
226 catgtcataactgaactgtgagaaaaacgccagttattttatggtacggg 275
   ||: : |: | :| || |||:| | | |:| |||:|
4543 canaancnangtanatttataaaganatgggaaattaantaatggna.... 4588
      .      .      .      .      .
276 attaatagggttccaaaaaccagccgtaacctattta....tattagggt 320
   ||: |:| ||| :| | | |: |:| | : | | |:|
4589 atnannaggaggattgnaacggtcnganccngnangaanagtttttannng 4638
      .      .      .      .      .
321 actttaagctggtgccctcagttttgttggtgtcttcgtttttaaaactta 370
   | | ||| | | | |:| | : | :| | | : |
4639 tttaaataactgggg.....gagtnagnagccngccnctggttcngtgta 4682
      .      .      .      .      .
371 gttgtatttttttcttagttctgtccttctagtggttatagagcataagg 420
   | :| | :| | :| | : |:| :| :| :| | | | |
4683 gangaaaccaagnnccggg...aggnttncannnnnaggggagaaaaaagg 4729
      .      .      .      .      .
421 acaaaattgagcaa.....aaaatgactaaggataaaaatgaggatgat 463
   |: | |:| :| :| | | | | | | | | | |
4730 anncatttnannangcngagggacatgaancggtacngagctgngggttca 4779
      .      .      .      .      .
464 cagaaagggcagcagcttaaaaaaaccttt.....tatattagttcaaaa 507
   :| :| | | :| :| :| | | :| :| | | | |
4780 nnnanccg.....cgnnnggnagtcccnngggacnngntggggttnanaa 4824
      .      .      .      .      .
508 ggacaccagtcataaaaaagtatactccaagcacatttgaatttggattt 557
   | | | : | | :| :| :| :| :| | | | |
4825 gggaanggaacattnggtngnangnganaaanaccttttcatnattgccttt 4874
      .      .      .      .      .
558 gcattgtcagtcaggccagtcgaaggggac 586

```

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||| :: : :|||: |: || :||
4875 gcaggnngtntngcncntncgggtnac 4903

Input Sequence: 1587_SEQ_1

!!NA_SEQUENCE 1.0
1587_SEQ_1 Length: 590 October 18, 2006 12:10 Type: N Check: 9861 ..

```
1  gaattcgccc ttggtagatg tctagatgac ctattctact tttcctaaga
51  ttttctctgt atgagtaacc tgtcataatt taacttgtga gatcttgccg
101 atataaaaaa aaaacgccag tcatttatgg tacgggatta ataggttcca
151 agaaccagcc acaatccatt tattagtctc atataaatgt cataaatttt
201 tactaaaatt ttctctgtat agtaacatgt cataactgaa cttgtgagaa
251 aaacgcagct tatttatggc acgggattaa taggttccaa aaaccagccg
301 taacctatct atattagggc actttaagct ggtgccctca gttttgttgg
351 tgtcttcggt tttaaactta gttgtatctt ttttcttagt tctgtccttc
401 tagtgttata gagcataaag acaaaattga gcaaaaaatg actaaggata
451 aaaatgagga tatcagaaaag gccagcagct taaaaaacct tttatattag
501 ttcaaaaagga caccagtcta taaaaagtat actccaagca catttgaatt
551 tggatttgca ttgtcagtca ggccagtcga ggggaccatg
```

Input Sequence: 6777591_SEQ_8

!!NA_SEQUENCE 1.0
6777591_SEQ_8 Length: 4999 December 15, 2006 17:07 Type: N Check: 1234
..

```
1  ctcaagcata cggacaaggg taaataacat agtcaccaga acataataaa
51  caaaaagtgc agaagcaaga taaaaaaatt agctatggac attcaggttc
101 atattggaaa catcattatc ctagtcttgt gaccatcctt cctcctgctc
```

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151 tagttgagag gccttgggac taacgagagg tcagttggga tagcagatcc
201 ttatcctgga ctagcctttc tgggtgttca gagtcttcgt gccgcgctct
251 acatctatct ccattaggtc tgaagatgac tcttcacacc aacgacgttt
301 aaggtctcta tcctactcct agcttgcaat acctggcttg caatacctgg
351 agcatcgtgc acgatgattg gatactgtgg aggaggagtg ttgtctgatt
401 tagagctccc ggttgggtga ttgacttcg atttcagttt aggcttgttg
451 aaatttttca ggttccattg tgaagccttt agagcttgag ctctcttcca
501 tgtaatatgcc ttgatcgaat tctcctagag aaaagggagc tcgatctctg
551 agtattgaaa tcgaagtgc aatttttttt caacgtgtcc aatcaatcca
601 caaacaagc agaagacagg taatctttca tactatact gacaagtaat
651 agtcttaccg tcatgcataa taacgtctcg ttcttcaag aggggttttc
701 cgacatccat aacgaccga agcctcatga aagcattagg gaagaacttt
751 tggttcttct tgtcatggcc tttataggtg tcagccgagc tcgccaattc
801 ccgtccgact ggctccgcaa aatattcgaa cggcaagtta tggacttgca
851 accataactc cacggtattg agcaggacct attgtgaaga ctcatctcat
901 ggagcttcag aatgtggttg tcagcaaacc aatgaccgaa atccatcaca
951 tgacggacgt ccagtgggtg agcgaacga aacaggaagc gcctatcttt
1001 cagagtcgtg agctccacac cggattccgg caactacgtg ttgggcaggc
1051 ttcgccgtat tagagatatg ttgaggcaag acccatctgt gccactcgta
1101 caattacgag agttgttttt tttgtgattt tcctaagttt ctcgttgag
1151 gtgagctcat attctacatc gtatggtctc tcaacgtcgt ttctgtcat
1201 ctgatatccc gtcatttgca tccacgtgag ccgcctcccg tgccaagtcc
1251 ctaggtgtca tgcacgcaa attggtggtg gtgcgggctg ccctgtgctt
1301 cttaccgatg ggtggagggt gagtttgggg gtctccgcgg cgatggtagt
1351 gggttgacgg tttggtgtgg gttgacggca ttgatcaatt tacttcttgc
1401 ttcaaattct ttggcagaaa acaattcatt agattagaac tggaaaccag
1451 agtgatgaga cggattaagt cagattccaa cagagttaca tctcttaaga

1501 aataatgtaa cccctttaga ctttatatat ttgcaattaa aaaaataatt
1551 taacttttag actttatata tagttttaat aactaagtgtt aaccactcta
1601 ttattttatat cgaactatt tgtagtctc ccctctaaat aaacttggtta
1651 ttgtgtttac agaactata atcaaataat caatactcaa ctgaagtgtg
1701 tgcagttaat tgaagggatt aacggccaaa atgcactagt attatcaacc
1751 gaatagattc acactagatg gccatttcca tcaatatcat cgccgttctt
1801 cttctgtcca catatcccct ctgaaacttg agagacacct gcacttcatt
1851 gtccttatta cgtgttacaa aatgaaacct atgcatccat gaaaactgaa
1901 gaatggcgca agaacccttc ccctccattt cttatgtggc gaccatccat
1951 ttcaccatct cccgtataaa aacaccccca tcacttcacc tagaacatca
2001 tcaactacttg cttatccatc caaaagatag ccaccatggc tagatcatca
2051 agccctttgc ttctctcact ctgcattttc gccattctct tccaactctc
2101 tctgggtagg cagcaattcc agcaggggaa cgagtgccag atcgacagga
2151 tcgacgcata cgagccggac aaaaccatcc aggcagaagc tggcaccatc
2201 gaggtatggg accagaaccg ccagcaattc cagtgcgctg gtgttgccgt
2251 tgtaaggcgc accattgagc ccaaaggctc tctcttgctt ttctacagca
2301 acacccctca gctcatctac atcgttcaag gtataaatta aatcagttca
2351 tacaatgata accaccactt cgaatgtatt tatcaaatat caatgatcga
2401 tgcacctgta tgtgttgtgt atattcaggt aggggagtta caggaatcat
2451 gttcccaakga tgtccagaga cattcgagga atcccagcag caaggacaac
2501 agggccaaca gggtagttcc caagaccagc accagaagat ccgccgcttc
2551 cgtgaagggt acgtcattgc cgtccctgcc ggtgtagccc actggtccta
2601 caacgatggc aacgaaccag tcatggccat tgttgccat gacacttcca
2651 gccacctcaa ccaactggac aacaacccca gggatatata gcattgccgt
2701 agttgctaataa aattgcaca caattggaac tctattttca gtatctaata
2751 actttttcct tttttggcag aacttctact tggcagggaaa cccgagagac
2801 gagttcgaac aatcgagca aggaggcagg ctgagccgtg gggagagtga

2851 aggtggacga ggacgcaggg aacctcttca acctgcaaca acctcttctt
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